REMARKS

This paper is filed in response to the notification of defective response mailed March 1, 2007. A copy of the NDR is enclosed.

Applicants requested national stage entry on December 27, 2004; the attachments included a paper copy only of a sequence listing (172 sequences).

On June 14, 2005, Applicants were mailed a "Notification to Comply with Requirements for... Sequence Disclosures". Applicants responded on August 12, 2005, by submitting a paper and CRF with the required statement. It is unclear whether this paper copy actually differed from the original one.

On November 6, 2006, Applicants were mailed a new Notification to Comply, which advised applicants that "claims 14-16 contain nucleic acid sequences with no sequence identifiers."

Applicants responded on January 8, 2007, submitting a new sequence listing, paper and CRF, with 216 sequences, and amending the specification and claims to provide SEQ ID Nos, and to point out certain errors in the November 6, 2006 paper.

The instant Notification of Defective Response stated that the CRF filed January 8, 2007 had been "found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report". The Report was not in fact attached and was not found in the IFW. Donna Greene, who signed the NDR, was asked by phone to provide a copy of the report, but did not provide such a copy. Hence we don't know the nature of the problem with the CRF (e.g., physically damaged, file missing, file in wrong format, file corrupt, etc.).

It has come to our attention that SEQ ID NOs:173, 176, 184, 187, 189 and 203 were not correctly presented in the January 8, 2007 sequence listing. We consulted with PTO sequence listing specialist Christopher Lowe on March 7, 2007, and these sequences have been reformatted in accordance with his recommendations. Naturally, this means that we are submitting the substitute sequence listing in both paper and CRF, attached hereto.

2. The undersigned attorney or agent hereby states as follows:

(a) this submission does not include new matter [§1.821(g)];

(b) the contents of the paper copy (as amended, if applicable) and the computer readable form of the Sequence Listing, are the same [§1.821(f) and §1.825(b)];

(c) if the paper copy has been amended, the amendment is supported by the specification and does not include new matter [§1.825(a)]; and

(d) if the computer readable form submitted herewith is a substitute for a form found upon receipt by the PTO to be damaged or unreadable, that the substitute data is identical to that originally filed [§1.825(d)].

3. Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no

association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Respectfully submitted,

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By: _____
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Enclosure
-paper Sequence Listing
-CRF

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IPC:lms
G:\ipc\g-i\hoib\Nexo1\pto resp notif.defect resp.wpd